

Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCELIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

1/46

ACGTTGACAC AGGAATGAAG AGTGTATTGG CTGAATCTTC AAGCAGAGGC GATATTGACC 60

ATGTGCTTT TAAATTGGCC TGC GTGACCC GCCCACTTGG TGTAAAAGAA GAACCGGCCA 120

AAGGGAGGGC CTGAAGGACC TCCACAGGAG TGTGAGGCAGC ACTGCTTCAG CAACAAAGCC 180

TCAGGGTCCAC ATCTTGGAA GAAT ATG GCC ACT TCC TGG GGG GCT GTC TTC 231
Met Ala Thr Ser Trp Gly Ala Val Phe
1 5
10 15

ATG CTG ATC ATA GCC TGC GTT GGC AGC ACT GTC TTC TAC AGA GAA CAG 279
Met Leu Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln
10 15
20 25

CAG ACC TGG TTT GAA GGT GTC TTC TTG TCT TCC ATG TGC CCC ATT AAT 327
Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn
30 35
35 40

GTC AGT GCC GGC ACC TTT TAT GGA ATT ATG TTT GAT GCG GGC AGC ACT 375
Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
45 50
50 55

GGA GCT CGG ATT CAT GTT ACT TTT GTG CAG AAA ACA GCA GGA CAG 423
Gly Ala Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln
60 65
65 70

FIG. 1A



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

2/46

ctc	ccc	ttt	ctg	gaa	ggg	att	ttt	gat	tct	gtg	aag	ccg	ggg	ctt	471
Leu	Pro	Phe	Leu	Glu	Gly	Glu	Ile	Phe	Asp	Ser	Val	Lys	Pro	Gly	Leu
75															85
TCT	GCT	TTT	GTG	GAT	CAG	CCC	AAA	CAG	GGT	GCT	GAG	ACT	GTC	CAG	519
Ser	Ala	Phe	Val	Asp	Gln	Pro	Lys	Gln	Gly	Ala	Glu	Thr	Val	Gln	Glu
90															105
CTC	TTG	GAG	GTG	GCC	AAA	GAC	TCG	ATC	CCC	AGA	AGC	CAC	TGG	GAA	AGG
Leu	Leu	Glu	Val	Ala	Lys	Asp	Ser	Ile	Pro	Arg	Ser	His	Trp	Glu	Arg
															120
95															
ACC	CCG	GTG	GTT	CTG	AAA	GCA	ACG	GCC	GGA	CTC	CGT	TTG	CTG	CCT	GAG
Thr	Pro	Val	Val	Leu	Lys	Ala	Thr	Ala	Gly	Leu	Arg	Leu	Ile	Pro	Glu
125															135
CAG	AAA	GCC	CAG	GCT	CTG	CTC	TTG	GAG	GTA	GAG	GAG	ATC	TTC	AAG	AAT
Gln	Lys	Ala	Gln	Ala	Leu	Leu	Leu	Glu	Val	Glu	Glu	Ile	Phe	Lys	Asn
140															150
TCA	CCT	TTC	CTG	GTC	CCA	GAT	GGC	AGC	GTT	AGC	ATC	ATG	GAT	GGG	TCC
Ser	Pro	Phe	Leu	Val	Pro	Asp	Gly	Ser	Val	Ser	Ile	Met	Asp	Gly	Ser
155															165

FIG. 1B



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEAR ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

3/46

TAT	GAA	GGC	ATA	CTA	GCC	TGG	GTT	ACC	GTC	AAC	TTT	CTA	ACA	GGT	CAG	759
Tyr	Glu	Gly	Ile	Leu	Ala	Trp	Val	Thr	Val	Asn	Phe	Leu	Thr	Gly	Gln	170
																175
																180
																185
CTG	CAT	GGT	CGT	GGC	CAG	GAG	ACT	GTG	GGG	ACC	CTT	GAC	CTG	GGG	GGT	807
Leu	His	Gly	Arg	Gly	Gln	Glu	Thr	Val	Gly	Thr	Leu	Asp	Leu	Gly	Gly	190
																195
																200
GCC	TCC	ACC	CAA	ATC	ACG	TTT	CTA	CCC	CAG	TTT	GAG	AAA	ACC	CTG	GAA	855
Ala	Ser	Thr	Gln	Ile	Thr	Phe	Leu	Pro	Gln	Phe	Glu	Lys	Thr	Leu	Glu	195
																210
																215
CAA	ACA	CCT	AGG	GGC	TAC	CTC	ACT	TCC	TTT	GAG	ATG	TTT	AAC	AGC	ACT	903
Gln	Thr	Pro	Arg	Gly	Tyr	Leu	Thr	Ser	Tyr	Leu	Gly	Phe	Asn	Ser	Thr	220
																225
																230
TTT	AAG	CTC	TAT	ACA	CAT	AGT	TAC	TTG	GGA	TTT	GGA	CTG	AAA	GCT	GCA	951
Phe	Lys	Leu	Tyr	Thr	His	Ser	Tyr	Leu	Gly	Phe	Gly	Leu	Lys	Ala	Ala	235
																240
																245
AGA	CTG	GCA	ACT	CTG	GGA	GCC	CTG	GAA	GCA	AAA	GGG	ACT	GAT	GGA	CAT	999
Arg	Leu	Ala	Thr	Leu	Gly	Ala	Leu	Glu	Ala	Lys	Gly	Thr	Asp	Gly	His	250
																260
																265

FIG. 1C



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

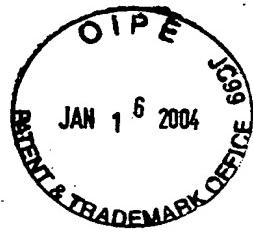
Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

4/46

ACG	TTT	CGA	AGT	GCC	TGT	TTA	CCA	AGA	TGG	TTG	GAA	GCA	GAG	TGG	ATC	1047
Thr	Phe	Arg	Ser	Ala	Cys	Leu	Pro	Arg	Trp	Leu	Glu	Ala	Glu	Trp	Ile	
																270
																275
																280
																285
																290
																295
																295
GGC	TTT	GAA	CCC	TGC	TAT	GCG	GAA	GTC	CTG	AGG	GTA	GTA	CAG	GGG	AAA	1095
Gly	Phe	Glu	Pro	Cys	Tyr	Gln	Tyr	Gly	Gly	Asn	Gln	Glu	Gly	Glu	Met	
																300
																305
																310
																310
																310
CTT	CAC	CAG	CCA	GAA	GTC	CGA	GGA	AGC	GCC	TTC	TAC	GCT	TTC	TCT	1143	
Leu	His	Gln	Pro	Glu	Glu	Val	Arg	Gly	Ser	Ala	Phe	Tyr	Ala	Phe	Ser	
																315
																320
																325
																325
TAC	TAC	TAC	GAT	CGA	GCC	GCT	GAC	ACA	CAC	TTG	ATC	GAT	TAT	GAA	AAG	1191
Tyr	Tyr	Tyr	Asp	Arg	Ala	Ala	Asp	Thr	His	Leu	Ile	Asp	Tyr	Glu	Lys	
																330
																335
																340
																340
GGC	GGG	GTT	TTA	AAA	GTT	GAA	GAT	TTT	GAA	AGA	AAA	GCC	AGA	GAA	GTG	1239
Gly	Gly	Val	Leu	Lys	Val	Glu	Asp	Phe	Glu	Arg	Lys	Ala	Arg	Glu	Val	
																350
																355
																360

FIG. 10



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

5/46

TGT	GAC	AAC	TTG	GGG	AGC	TTC	TCC	TCG	GGC	AGT	CCT	TTC	CTC	TGC	ATG	1335	
Cys	Asp	Asn	Leu	Gly	Ser	Phe	Ser	Ser	Gly	Ser	Pro	Phe	Leu	Cys	Met	365	
																370	
GAC	CTC	ACT	ATC	ACA	GCC	CTG	TTG	AAA	GAT	GGT	TTG	GGC	TTT	GCC	1383		
Asp	Leu	Thr	Tyr	Ile	Thr	Ala	Leu	Leu	Lys	Asp	Gly	Leu	Gly	Phe	Ala	380	
																385	
GAA	CGG	CAC	CCT	CTT	ACA	GCT	CAC	AAA	GAA	AGT	GAA	CAA	CAT	AGA	GAC	1431	
Glu	Arg	His	Pro	Leu	Thr	Ala	His	Lys	Glu	Ser	Glu	Gln	His	Arg	Asp	395	
																400	
TGG	TTG	GGC	CTT	GGG	GGC	CAC	CTT	TCA	CCT	GCT	CCA	GTC	TCT	GGG	CAT	1479	
Trp	Leu	Gly	Leu	Gly	Gly	His	Leu	Ser	Pro	Ala	Pro	Val	Ser	Gly	His	410	
																415	
																420	
CAC	CAG	CTG	AGG	CCA	AGC	TCC	ACC	TCT	GAA	GCC	TGC	ATT	TCT	GAA	CCA	1527	
His	Gln	Leu	Arg	Pro	Ser	Ser	Thr	Ser	Glu	Ala	Cys	Ile	Ser	Glu	Pro	430	
																435	
GTT	TTC	TCA	CAG	GAA	GGC	GTG	GAC	TCA	GAG	ACA	TTT	TCT	GAC	CTC	TCT	1575	
Val	Phe	Ser	Gln	Glu	Gly	Val	Asp	Ser	Glu	Thr	Phe	Ser	Asp	Leu	Ser	445	
																450	
																455	

FIG. 1E



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEAR ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

6/46

GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTT TATAAGGAGG GAGGGTTT 1629
Gly Lys Ala Trp Pro Glu Thr Arg
460 465

TAGATGAGTC TTGCTCTTGA GCCTAGTGAT TTGGGCTCA ATGATTGCA CATCTAATGT 1689
GAATAGCTCC TAACCACTTG GTGGGTGCAT GGCTGGCACC AGACTGTAAA TCTTTGGGA 1749
TTCTTTGTAC AGAGTCCTGC AAAGAAAAAA AGAGAAAAAGG TTTGGAACTC CATGCTAGAT 1809
TGCAGATTCA GAGACAGGTC CCTGGGGACC AAAGAACAAAT CTCGTTCAA CCCTTGGATG 1869
CCTCATGCT TTGAATGGAT TCATTGGTC TTATAAGCTG ATTACTGAA ATCCCATAAC 1929
CCATCAATGCG TGTTAATTTC TTTCTTCTTA CCCTTATTAC ATTCCCTTAC CTAAAAGCCT 1989
GGGGAAATA CCTGGTTTG CTTCCCCATCT ATAATGAGA AAGAGGGGG AAAAGATACT 2049
GTATTAGAAAT TTGTGTGATC CTGTGGCACA ATAGATCAAC CAACCCATT AAAGCTTAAA 2109
AAAAAAAAAA 2119

FIG. 1F



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

7/46

peaNTPase	1	- - - MELLIKLITFLFSMPAITS S Q Y L G N N L L T S R K I F L K Q E E I S S Y A V V F D A G S T G S R
potapyrase	1	M L N Q N S H F I F I L L A I F F L V L P L S L L S K N V N A Q I P L R R H L L S H E S E - - H Y A V I F D A G S T G S R
mNTPase	1	M A T S W G A V F M L L I A C V G S T V F Y R E Q Q T W F E G V F L L S M C P I N V S A G T F Y G I M F D A G S T G T R
yGDPase	1	K T P E D I S I L P V N D E P G Y L Q D S K T E Q N Y P E L A D A V K S Q T S Q T C S E E H K Y V I M I D A G S T G S R
peaNTPase	57	I H V Y H F N O N L D L L H I I G K G V E R Y Y N K I T P G L S S Y A N N P E Q A A K S L I P L L E Q A E D V V P D D L Q P
potapyrase	59	V H V F R F D E K L G L L P I G N N I E Y F M A T E P G L S S Y A E D P K A A A N S L E P L L D G A E G V V P Q E L Q S
mNTPase	61	I H V Y T F V Q K T A G Q L P F L E G E I F D S V K P G L S A F V D Q P K Q G A E T V Q E L L E V A K D S I P R S H W E
yGDPase	61	V H I Y K F D V C T S - - P P T L L D E K F D M L E P G L S S F D T D S V G A A N S L D P L L K V A M N Y V P I K A R S
peaNTPase	117	K T P V R L G A T A G L R L L N G D A S E K I L Q S V R D M L S N R S T F - N V Q P D A V S I I D G T Q E G S Y L W V T
Potapyrase	119	E T P L E L G A T A G L R M I K G D A A E K I L Q A V R N L V K N Q S T F - H S K D Q W V T I I D G T Q E G S Y M W A A
mNTPase	121	R T P V V L K A T A G L R L L P E Q K A Q A L L E V E E I F K N - S P F - L V P D G S V S I M D G S Y E G I L A W V T
yGDPase	119	C T P V A V K A T A G L R L L G D A K S S K I L S A V R D H L E K D Y P F P V V E G D G V S I M G G D E E G V F A W I T

FIG. 2A



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

8/46

peaNTPase	176	VNYALGNL G KYTK - - TVGVIDLG GGSVQ MAYAVSKTAKNAPKVA DGGDDPYIKR VVLKG
potapyrase	178	INYLLG N L G D Y K S - - T T ATIDLG GGSVQ MAYAI SNEQF A KAPQNEDG - E PYVQQ KHLM S
mNTPase	179	VNF L T GQ L H G R G Q E - - TVGT IDLG G ASTQ ITFLP QFEK - - - T LEQT PRGYLT SFEMFN
yGDPase	179	TNYLLG N I G ANG P K L P TAAV F DLG GG STQ IV FE P - - T FPI NE KM V DGEHKF - - DLKF GD
peaNTPase	234	I PYDLYVHSY YLHF FGREASRAEILKL - - - - - T PRSPNP C LLAGFNGI Y
potapyrase	235	K DYNLYVHSY LN YGQLAGRAEIFKA - - - - - S RNESNP CA LEGCDGY
mNTPase	232	S TEFKLYTHSY LG FFGLKAA RLAT LGA - - - - - LEAK GT - - - D GHTFRS
yGDPase	234	E NYTLYQFSHLG Y GYGLKEGRNKVN SV LVENA LKD GKILK GDNT KTHQLSSP C LPPPKVNATN
peaNTPase	276	T YSGEEF K ATA YT SGA - - - - N ENKCKNTIRK ALKLN YP C PYQ <u>N</u> CTF GG LIWNGGGN - - -
potapyrase	277	S XGGV D YKVKAPKKG S - - - - SWK R C RR L TR H ALKINA K CNIE <u>E</u> CTF NG VWNGGGD - - -
mNTPase	270	A CLP R W LE A E W I F GG V - - - - KYQ Y GG NQE <u>GFEPCYAEVLRVVQ<u>GKLHQPEEVR - - -</u></u>
yGDPase	294	E KV T LES K ETY T IDFIGPDEPSGAQ C Q <u>SPPC<u>SFNGVHQPSLVRTFK</u></u>

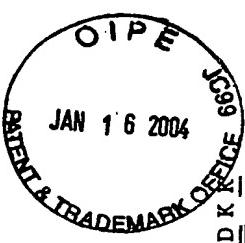
FIG. 2B

Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEAR ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

9/46



peaNTPase 328 G Q K N L P A S S F F Y L P E D T G M V D A S T P N F I L R P V D I E T K A K E A C A L N F E D A K S T Y P F L D K R D E
potapyrase 329 G Q K N I H A S S F F Y D I G A Q V G I V D T K F P S A L A K P I Q Y L N A A K V A C Q T N V A D I K S I F P K T Q D R
mNTPase 322 G S A - F Y A P S Y Y D R A A D T H L I D Y E - K G G V L K V E D F E R K A R E V C D - N L G S F S S G S P - - -
yGDPase 354 E S N D I Y I F S Y F Y D R T R P L G M P L S F T L N E L N D L A R I V C K G E E T W N S V F S C I A G S - - L D E L

peaNTPase 388 N V A S S Y V C M D L I Y Q Y V V L V D G F G L D P L Q K I T S C K E I E Y Q D A I V E A A W P L G N A V E A I S A L P K
potapyrase 389 N I - P Y L C M D L I Y E Y T L L V D G F G L N P H K E I T V I H D V Q Y K N Y L V G A A W P L G C A I D L V S S T T N
mNTPase 374 - - - F L C M D L T Y I T A L L K D G I G F A E R H P L T A H K E S E Q H R D W L G L G G H L S P A P V S G H H Q L R
yGDPase 411 E S D S H F C L D L S F Q V S L L H T G Y D I P L Q R E L R T G K K I A N K E - - - I G W C L G A S L P L L K A D N W

peaNTPase 448 F E R L M Y F V

potapyrase 448 K I R V A S S *

mNTPase 430 P S S T S E A C I S E P V F S Q E G V D S E T F S D L S G K A W P E T R *

yGDPase 467 K C K I Q S A

FIG. 2C



**Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS**

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

10/46

FIG. 3A



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

11/46

ACR II

		<u>KP - VQKVNEIGI - YLTDCMERAREVIPR - - S - QHQETPVYLGATAGMRLLLRMESSEELAD</u>
ratCD39	47	<u>KY - AQKTDEIAA - YLAECMKMSTERIPA - - SKQHQ - TPVYLGATAGMRLLLRMESKQSAD</u>
CD39L1	47	<u>SY - ADNPSGASQ - SLVGCLEQALQDVPK - - ER - HACTPLYLGATAGMRLLNLTNP EAST</u>
chiATPase	47	<u>SY - SS SKPPAAGK - SLEHCLSQAMRDVPK - - EK - HADTPLYLGATAGMRLLTIA DPPSQT</u>
peaNTPase	46	<u>SY - ANNPEQAAKS - LIPPLEQAEDVVVP - - DLQPKTPVRLGATAGLRLNN - - GDA - SE</u>
potRROPL	46	<u>SY - AEDPKAAANS - LEPLLDDGAEGGVVP - - QELQSETPLELGATAGLRLRMLK - - GDA - AE</u>
yGDA1	44	<u>S PDTDSSV - GAANS - LDPLLKVAMNYVPI - - KARSCTPVAVKATAAGLRLL - - GDAKSS</u>
mNTPase	46	<u>AP - VDQPKQGAET - VQELLEVAKDSI PRSHWE - - R - - TPVVLKATAAGLRLL - - PEQKAQ</u>
hCD39L2	10	<u>AY - ADDVEKSAQG - IRELLDVAKQDIP - - FDSSGRP - TPLVLKATAAGLRLL - - PG EKAQ</u>
c elegans	51	<u>SFG - DKPEQVVE - YLTPLLRFEEHIPYEQLGE - - TDLLIFATAGMRLLL - - PEAQKD</u>
y71KD	61	<u>SFE - KK PQQDAYKSHIKP LLDFAKNLIPESHWS S - - CPVFIQATAGMRLLL - - PQDIQS</u>

FIG. 3B



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

12/46

ACR III

CD39	101	R V L D V V E R S L S S N - Y P F - - - - - D F Q G A R I I T G Q B E G A Y G W I T I N Y L L G K F S Q K T R W F S I V P
ratCD39	101	E V L A A V S R S L K S - Y P F - - - - - D F Q G A K I I T G Q E E G A Y G W I T I N Y L L G R F T Q E Q S W L N F I S
CD39L1	101	S V L M A V T H T L T Q - Y P F - - - - - D F R G A R I I L S G Q E E G V F G W V T A N Y L L E N F I - K Y G W V G - - R
chiatPase	101	- C L S A V M A T L K S - Y P F - - - - - D F G G A K I I L S G C E E E G V F G W I T A N Y L L E N F I - K R G W L G - - E
peantPase	97	K I L Q S V R D M L S N R S T F N - V Q P D - A - V S I I D G T Q E C S Y L W V T V N Y A L G N - - - - - L - - - G
potRRop1	97	K I L Q A V R N L V K N Q S T F H - - S K D - Q W V T I L D G T Q E G S Y M W A A I N Y L L G N - - - - - L - - - G
YGDA1	95	K I L S A V R D H L E K D Y P P P V V E G D - G - V S I M G G D E E G V F A W I T T N Y L L G N - - - - - I G A N G
mNTPase	97	A L L L E V E E I P - K N S P F - L V - P D - G S V V S I M D G S Y E G I L A W V T V N F L T G Q - - - - - L H G R G
hCD39L2	61	K L L Q K V K E Y L - K H S P F - L V - G D - D C V S I M N G T D E G V S A W X T I N F L T G S - - - - - L K T P G
celegans	102	A L I K N L Q N G L K S V T A L R V S D - - - S N I R I I D G A W E G I Y S W I A V N Y I L G R - - - - - F - D - -
Y71KD	113	S I L D G L C Q G L K H P A E F L V E D C S - A Q I Q V I D G E T G L Y G W L G L N Y L Y G H - - - - - F N D Y N

FIG. 3C



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

13/46

ACRIV

CD39	155	<u>YETNNQETFPGALD</u> <u>LGCASTQVTFVPQNQ</u>
ratCD39	155	- <u>DSSQKQATFPGALD</u> <u>LGGSSTQVTFVPLNQ</u>
CD39L1	152	<u>WFRPRKGTLGAMDLGGAS</u> <u>TQITFETTSP</u>
chiATPase	151	<u>WIQSKKKTTLGAMDFGGAS</u> <u>TQITFETSDAI</u>
peaNTPase	144	<u>KKYTK - - TVGVIDLGGGS</u> <u>VQMAVAVSKK</u>
potRRP01	144	<u>KDYKS - - TTATIDLGGS</u> <u>VQMAVAYAISNE</u>
YGDA1	146	<u>PKL - P - - TAAVFDLGGGSTQIVFEP</u> <u>PTPP</u>
mNTPase	146	<u>QE - - - TVGTTLDLGGAS</u> <u>TQITFLPQFE</u>
hCD39L2	110	<u>GS - - - S VGMLDLGGGSTQIAFLP</u> <u>RVE</u>
celegans	149	<u>KE - NDS - KVGMIDMGGASVQIAFEIA - NE</u>
Y71KD	165	<u>PEVSDHFTFGFMDDMGCASTQIAF - - APHD</u> <u>S</u>

FIG. 3D



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

14/46

GTGGGGTCGT	ATCCCCGGG	TGGAGGCCGG	GGTGGGCCGG	GCCGGGCCGG	GGGAGCCCAA	60
AAGACCGGGCT	GCCGCCTGCT	CCCCGGAAA	GGGCACACTCGT	CTCCGTGGGT	GTGGGGAGC	120
GCGCGGTGCA	TGGAATGGGC	TATGTGAATG	AAAAAAGGTA	TCCGTATGA	AACTTCCAGA	180
AAACAGAGCT	ACATTTCA	GCAGCCGCAG	CACGGTCCTT	GGCAAACAAG	G ATG AGA	237
				Met	Arg	
			1			
AAA ATA TCC AAC CAC GGC CTG CGG GCG AAG GTG GCA TAC CCC						285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro						
5		10		15		
CTG GGG CTG TGT GTG GGC GTG RTC ATC TAT GTT GCC TAC ATC AAG TGG						333
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp						
20		25		30		
CAC CGG GCC ACC GCC ACC CAG GCC TTC AGC ATC ACC AGG GCA GCC						381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala						
35		40		45		
					50	

FIG. 4A



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

15/46

CCC	GGG	GCC	CGG	TGG	GGT	CAG	CAC	GCC	CCC	CTG	GGG	ACA	GCT	429		
Pro	Gly	Ala	Arg	Trp	Gly	Gln	Gln	Ala	His	Ser	Pro	Leu	Gly	Thr	Ala	
															55	
															60	
															65	
GCA	GAC	GGG	CAC	GAG	GTC	TTC	TAC	GGG	ATC	ATG	TTT	GAT	GCA	GGA	AGC	477
Ala	Asp	Gly	His	Glu	Val	Phe	Tyr	Gly	Ile	Met	Phe	Asp	Ala	Gly	Ser	
																70
															75	
															80	
ACT	GGC	ACC	CGA	GTA	CAC	GTC	TTC	CAG	TTC	ACC	CGG	CCC	CCC	AGA	GAA	525
Thr	Gly	Thr	Arg	Val	His	Val	Phe	Gln	Phe	Thr	Arg	Pro	Pro	Arg	Glu	
																85
															90	
															95	
ACT	CCC	ACG	TTA	ACC	CAC	GAA	ACC	TTC	AAA	GCA	GTG	AAG	CCA	GGT	CTT	573
Thr	Pro	Thr	Leu	Thr	His	Glu	Thr	Phe	Lys	Ala	Val	Lys	Pro	Gly	Leu	
																100
															105	
															110	
TCT	GCC	TAT	GCT	GAT	GTT	GAA	AAG	AGC	GCT	CAG	GGA	ATC	CGG	GAA	621	
Ser	Ala	Tyr	Ala	Asp	Asp	Val	Glu	Lys	Ser	Ala	Gln	Gly	Ile	Arg	Glu	
																115
															120	
															125	
															130	

FIG. 4B



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEAR ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

16/46

CTA	CTG	GAT	GTT	GCT	AAA	CAG	GAC	ATT	CCG	TTC	GAC	TTC	TGG	AAG	GCC	669	
Leu	Leu	Asp	Val	Ala	Lys	Gln	Asp	Ile	Pro	Phe	Asp	Phe	Trp	Lys	Ala		
																145	
																140	
ACC	CCT	CTG	GTC	CTC	AAG	GCC	ACA	GCT	GGC	TTA	CGC	CTG	TTA	CCT	GGA	717	
Thr	Pro	Leu	Val	Leu	Lys	Ala	Thr	Ala	Gly	Leu	Arg	Leu	Leu	Pro	Gly		
																150	
																155	
GAA	AAG	GCC	CAG	CAG	AAG	TTA	CTG	CAG	AAG	GTG	AAA	GAA	GTA	TTT	AAA	GCA	765
Glu	Lys	Ala	Gln	Lys	Leu	Leu	Gln	Lys	Val	lys	Glu	Val	Phe	Lys	Ala		
																160	
																170	
																175	
TCG	CCT	CTT	GTA	GGG	GAT	GAC	TGT	GTT	TCC	ATC	ATG	AAC	GGA	ACA	813		
Ser	Pro	Phe	Leu	Val	Gly	Asp	Asp	Cys	Val	Ser	Ile	Met	Asn	Gly	Thr		
																180	
																185	
GAT	GAA	GGC	GTT	TCG	GCG	TGG	ATC	ACC	ATC	AAC	TTC	CTG	ACA	GGC	AGC	861	
Asp	Glu	Gly	Val	Ser	Ala	Trp	Ile	Thr	Ile	Asn	Phe	Leu	Thr	Gly	Ser		
																195	
																200	
TTG	AAA	ACT	CCA	GGA	GGG	AGC	AGC	GTG	GGC	ATG	CTG	GAC	TTG	GGC	GGA	909	
Leu	Lys	Thr	Pro	Gly	Gly	Ser	Ser	Val	Gly	Met	Leu	Asp	Leu	Gly	Gly		
																215	
																220	
																225	

FIG. 4C



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCELIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

17/46

GGA	TCC	ACT	CAG	ATC	GCC	TTC	CTG	CCA	CGC	GTG	GAG	GGC	ACC	CTG	CAG	957
Gly	Ser	Thr	Gln	Ile	Ala	Phe	Leu	Pro	Arg	Val	Glu	Gly	Thr	Leu	Gln	230
																235
GCC	TCC	CCA	CCC	GGC	TAC	CTG	ACG	GCA	CTG	CGG	ATG	TTT	AAC	AGG	ACC	1005
Ala	Ser	Pro	Pro	Gly	Tyr	Leu	Thr	Ala	Leu	Arg	Met	Phe	Asn	Arg	Thr	245
																250
TAC	AAG	CTC	TAT	TCC	TAC	AGC	TAC	CTC	GGG	CTC	GGG	CTG	ATG	TCG	GCA	1053
Tyr	Lys	Leu	Tyr	Ser	Tyr	Ser	Tyr	Leu	Gly	Leu	Gly	Leu	Met	Ser	Ala	260
																265
CGC	CTG	GCG	ATC	CTG	GGC	GGC	GTG	GAG	GGG	CAG	CCT	GCT	AAG	GAT	GGA	1101
Arg	Leu	Ala	Ile	Leu	Gly	Gly	Val	Glu	Gly	Gln	Pro	Ala	Lys	Asp	Gly	275
																280
AAG	GAG	TTG	GTC	AGC	CCT	TGC	TTG	TCT	CCC	AGT	TTC	AAA	GGA	GAG	TGG	1149
Lys	Glu	Leu	Val	Ser	Pro	Cys	Leu	Ser	Pro	Ser	Phe	Lys	Gly	Glu	Trp	295
																300
GAA	CAC	GCA	GAA	GTC	ACG	TAC	AGG	GTT	TCA	GGG	CAG	AAA	GCA	GCG	GCA	1197
Glu	His	Ala	Glu	Val	Thr	Tyr	Arg	Val	Ser	Gly	Gln	Lys	Ala	Ala	Ala	310
																320

FIG. 4D



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCELIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

18/46

AGC	CTG	CAC	GAG	CTG	TGT	GCT	GCC	AGA	GTG	TCA	GAG	GTC	CTT	CAA	AAC	1245
Ser	Leu	His	Glu	Leu	Cys	Ala	Ala	Arg	Val	Ser	Glu	Val	Leu	Gln	Asn	
																325
																330
																335
AGA	GTG	CAC	AGG	ACG	GAG	GAA	GTG	AAG	CAT	GTG	GAC	TTC	TAT	GCT	TTC	1293
Arg	Val	His	Arg	Thr	Glu	Glu	Val	Lys	His	Val	Asp	Phe	Tyr	Ala	Phe	
																340
																345
TCC	TAC	TAT	TAC	GAC	CTT	GCA	GCT	GGT	GTG	GGC	CTC	ATA	GAT	GCG	GAG	1341
Ser	Tyr	Tyr	Tyr	Asp	Leu	Ala	Ala	Gly	Val	Gly	Leu	Ile	Asp	Ala	Glu	
																355
																360
																365
AAG	GGA	GGC	AGC	CTG	GTG	GGG	GAC	TTC	GAG	ATC	GCA	GCC	AAG	TAC	1389	
Lys	Gly	Gly	Ser	Leu	Val	Gly	Asp	Phe	Glu	Ile	Ala	Ala	Lys	Tyr		
																375
																380
																385
GTG	TGT	CGG	ACC	CTG	GAG	ACA	CAG	CCG	CAG	AGC	CCC	TTC	TCA	TGC	1437	
Val	Cys	Arg	Thr	Leu	Glu	Thr	Gln	Pro	Gln	Ser	Ser	Pro	Phe	Ser	Cys	
																390
																395
ATG	GAC	CTC	ACC	TAC	GTC	AGC	CTG	CTA	CTC	CAG	GAG	TTC	GGC	TTT	CCC	1485
Met	Asp	Leu	Thr	Tyr	Val	Ser	Leu	Leu	Leu	Gln	Glu	Phe	Gly	Phe	Pro	
																405
																410
																415

FIG. 4E



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

19/46

AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC 1533
Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
420 425 430

AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA 1581
Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
435 440 445 450

CAG AAG AGT CCA GCC TCA TAGTGGCGA GCCATCCCTG TCCCCGTCA
Gln Lys Ser Pro Ala Ser
455

CAGTGTCTGT GTGTCTGCAT AAACCCCTCCT GTCCCTGGACG TGACTTCATC CTGAGGAGCC 1689

ACAGCACAGG CCGTGCTGGC ACTTTCTGCA CACTGGCTCT GGGACTTGCA GAAGGCCTGG 1749

TGCTGCCCTG GCATCAGCCT CTTCCAGTCA CATCTGGCCA GAGGGCTGTC TGGACCTGGG 1809

CCCTGCTCAA TGCCACCTGT CTGCCCTGGC TCCAAGTGGG CAGGACCAGG ACAGAACAC 1869

AGGCACACAC TGAGGGGCA GTGTGGCTCC CTGCCTGTCC CATCCCCATG CCCCGTCCGC 1929

FIG. 4F



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCELIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

20/46

GGGGCTGTGG CTGCTGCTGT GCATGTCCT GCGATGGGAG TCTTGTCTCC CAGCCTGTCA 1989
GTTTCCTCCC CAGGGCAGAG CTCCCCCTTCC TGCAAGAGTC TGGGAGGG TAGCAGGCTGT 2049
CCTGGCTGCT CTGGGAAGC CGAGGGACAG CCATAAACACC CCCGGGACAG TAGGTCTGGG 2109
CGGCACCACT GGGAACTCTG GACTTGAGTG TGTTTGCTCT TCCTTGGTA TGAATGTGTG 2169
AGTTCACCCA GAGGCCTGCT CTCCTCACAC ATTGTGTGGT TTGGGGTTAA TGATGGAGGG 2229
AGACACCTCT TCATAGACGG CAGGTGCCA CCTTCAGGG AGTCTCCCAG CATGGGGGA 2289
TCCGGGCAT GAGCTGCTGT AAACATTG TGCTGTGCT GCTTGAGTGA CGTCTCTGTC 2349
GTGTGGTGC CAAGTGCCTTG TGTAGAAACT GTGTTCTGAG CCCCTTTTC TGGACACCAA 2409
CTGTGTCTG TGAATGTATC GCTACTGTGA GCTGTTCCCG CCTAGCCAGG GCCATGTCTT 2469
AGGTGCAGCT GTGCCACGGG TCAGCTGAGC CACAGTCCCCA GAACCAAGCT CTCGGTGTCT 2529

FIG. 4G



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

21/46

CGGCCACCA TCCGCCACC TCGGGCTGAC CCCACCTCCT CCATGGACAG TGTGAGCCCC 2589
GGCCGTGCA TCCTGCTCAG TGTGGGTCA GTGTCGGGC TGAGCCCTT GAGCTGCTTC 2649
AGTGAATGTA CAGTGCCCGG CACGAGCTGA ACCTCATGTG TTCCACTCCC AATAAAAGGT 2709
TGACAGGGC TTCTCCTTCA AAAAAAAA AAAAAAAA AAAA 2762

FIG. 4H



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEAR ACIDS
Applicants: Brian Paul Chadwick et al.
Docket No.: 28110/36120A
22/46

FIG. 5A

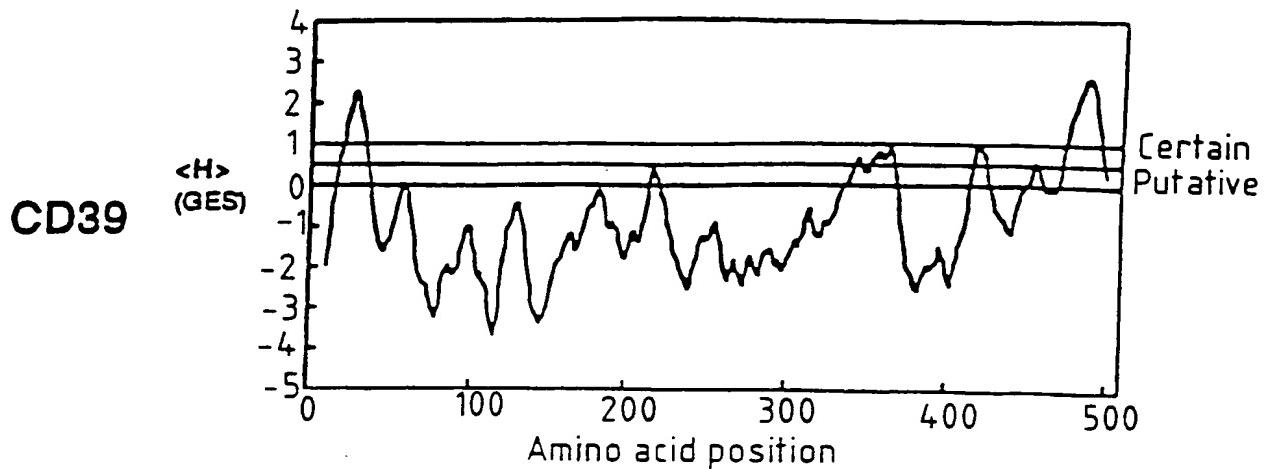


FIG. 5B

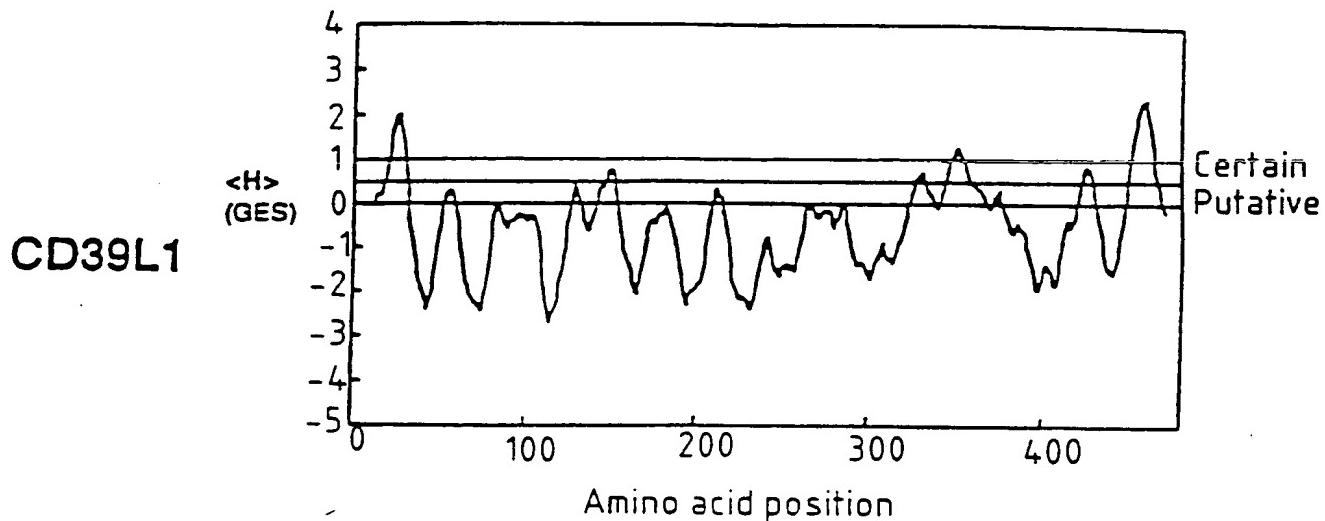
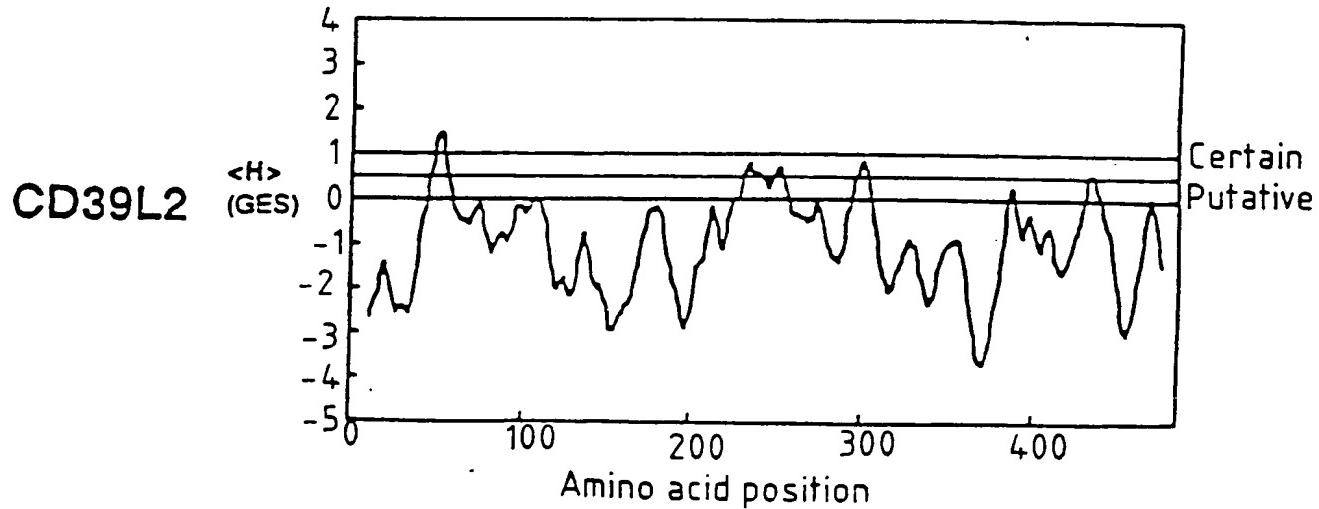


FIG. 5C





Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEAR ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

23/46

FIG. 5D

CD39L3

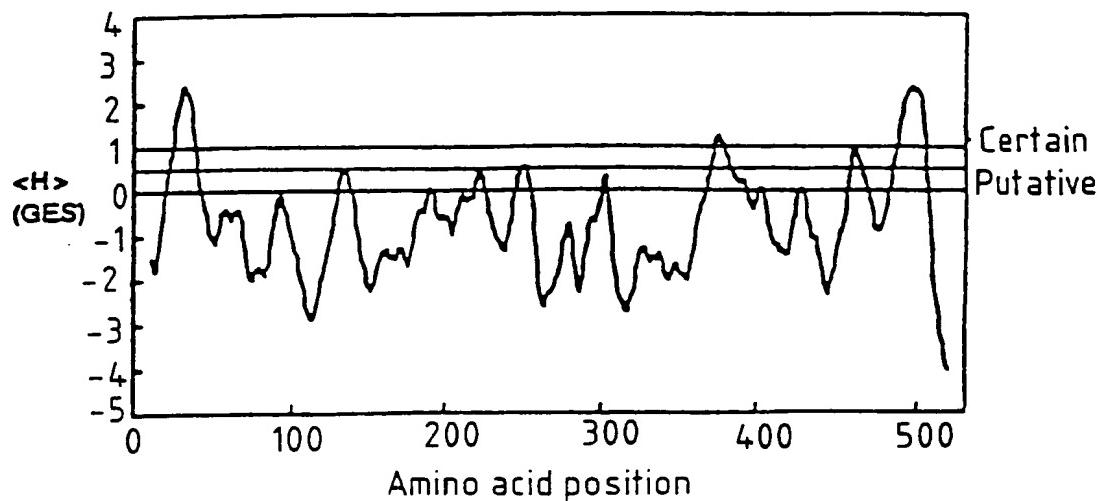
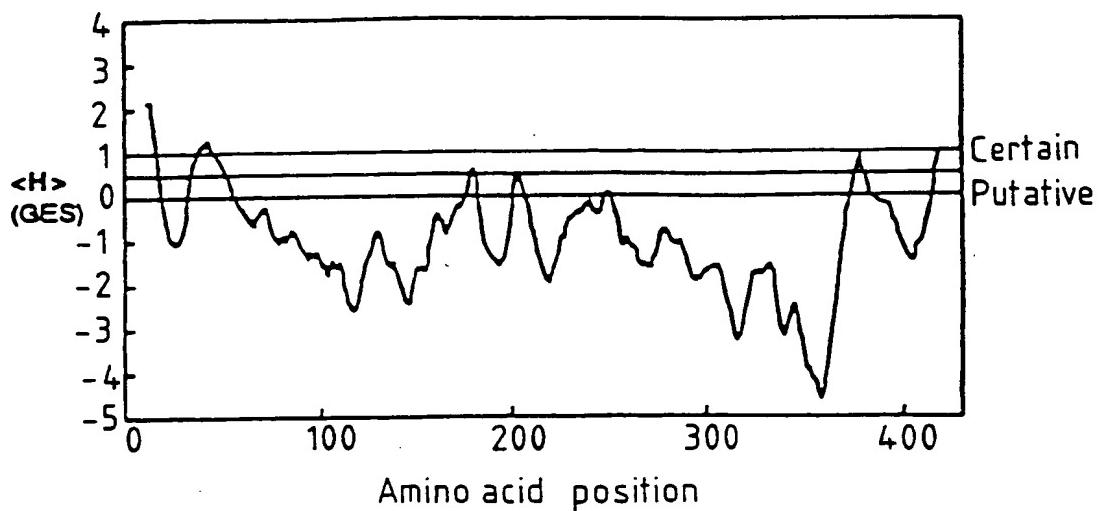


FIG. 5E

CD39L4





Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

24/46

ACCCACGGGT	CTGGCCGGG	GCCGCCCTTG	CGGCAGCGCT	AGTCGCCCTC	TCCGAATCGG	60
CTCCGCACAG	CTAGGAGAAA	AG	ATG TTC	ACT	GTG CTG ACC CGC CAA CCA TGT	112
			Met Phe	Thr Val	Leu Thr Arg Gln Pro Cys	
1				5		10
GAG CAA GCA	GGC CTC AAG GCC CTC	TAC CGA ACT CCA ACC ATC ATT GCC				160
Glu Gln Ala	Gly Leu Lys Ala	Leu Tyr Arg Thr Pro Thr Ile Ile Ala				
15				25		
TTG GTG GTC	TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC					208
Leu Val Val	Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val					
30		35		40		
ATC CAG ATC	CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT					256
Ile Gln Ile	His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly					
45		50		55		
ATT GTG CTG GAT	GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA					304
Ile Val Leu Asp	Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln					
60		65		70		

FIG. 6A



**Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEAR ACIDS**

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

25/46

FIG. 6B



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEAR ACIDS

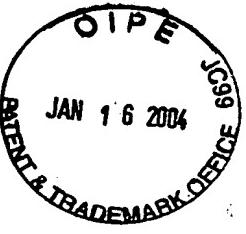
Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

26/46

Phe	Arg	Gly	T	TTT	AGG	GGT	GCT	CAA	ATC	ATT	TCT	GGG	CAA	GAA	GAA	GGG	GTA	TAT	GGA	640					
			Ile	175									Gln	Ile	Ser	Gly	Gln	Glu	Gly	Val	Tyr	Gly	185		
Trp	Ile	Thr	A	TGG	ATT	ACA	GCC	AAC	TAT	TTA	ATG	GGA	AAT	TTC	CTG	GAG	AAC	AAC	CTG	688					
			Ala	190									Tyr	Leu	Met	Gly	Asn	Phe	Leu	Glu	Lys	Asn	Leu	200	
Trp	His	Met	T	TGG	CAC	ATG	TGG	GTG	CAC	CCG	CAT	GCA	GTG	GAA	ACC	ACG	GGT	GCC	CTG	736					
			Trp	205									Val	Pro	His	Gly	Val	Glu	Thr	Thr	Gly	Ala	Leu	215	
GAC	TTA	GGT	G	GAC	TCA	TCC	ACC	CAA	ATA	TCC	TTC	GTG	GCA	GGA	GAG	GGT	GCC	CTG	AAG	784					
			Gly	220									Ala	Ser	Thr	Gln	Ile	Ser	Phe	Val	Ala	Gly	Glu	Lys	230
Asp	Leu	Gly	A	ATG	GAT	CTG	AAC	ACC	GAC	ATC	ATG	CAG	GTG	TCC	CTG	TAT	GGC	GAG	AAG	784					
			Asp	235									Asn	Thr	Ser	Asp	Ile	Met	Gln	Val	Ser	Leu	Tyr	Tyr	245
Val	Tyr	Thr	H	GTA	TAC	ACG	CTC	TAC	ACA	CAC	AGC	TTC	CAG	TGC	TAT	GGC	CGG	AAT	GAG	880					
			Leu	255									His	Ser	Phe	Gln	Cys	Tyr	Gly	Arg	Asn	Glu	265		

FIG. 6C



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEAR ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

27/46

GCT	GAG	AAG	AAG	TTT	CTG	GCA	ATG	CTC	CTG	CAG	AAT	TCT	CCT	ACC	AAA	928
Ala	Glu	Lys	Lys	Phe	Leu	Ala	Met	Leu	Leu	Gln	Asn	Ser	Pro	Thr	Lys	
																270
																275
AAC	CAT	CTC	ACC	AAT	CCC	TGT	TAC	CCT	CGG	GAT	TAT	AGC	ATC	AGC	TTC	976
Asn	His	Leu	Thr	Asn	Pro	Cys	Tyr	Pro	Arg	Asp	Tyr	Ser	Ile	Ser	Phe	
																285
ACC	ATG	GGC	CAT	GTA	TTT	GAT	AGC	CTG	TGC	ACT	GTG	GAC	CAG	AGG	CCA	1024
Thr	Met	Gly	His	Val	Phe	Asp	Ser	Leu	Cys	Thr	Val	Asp	Gln	Arg	Pro	
																300
GAA	AGT	TAT	AAC	CCC	AAT	GAT	GTC	ATC	ACT	TTT	GAA	GGA	ACT	GGG	GAC	1072
Glu	Ser	Tyr	Asn	Pro	Asn	Asp	Val	Ile	Thr	Phe	Glu	Gly	Thr	Gly	Asp	
																315
CCA	TCT	CTG	TGT	AAG	GAG	AAG	GTG	GCT	TCC	ATA	TTT	GAC	TTC	AAA	GCT	1120
Pro	Ser	Leu	Cys	Lys	Glu	Lys	Val	Ala	Ser	Ile	Phe	Asp	Phe	Lys	Ala	
																335
TGC	CAT	GAT	CAA	GAA	ACC	TGT	TCT	TTT	GAT	GGG	GTT	TAT	CAG	CCA	AAG	1168
Cys	His	Asp	Gln	Glu	Thr	Cys	Ser	Phe	Asp	Gly	Val	Tyr	Gln	Pro	Lys	
																350
																360

FIG. 6D



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEAR ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

28/46

ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC ACA GCC AGT
Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser
365 370 375

GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC
Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser
380 385 390

ACC TGG AAT TTC TGC TCA CAG AAT TGG AGT CAG CTC CCA CTG CTG CTC
Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu
395 400 405

CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC
Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn
415 420 425

TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT
Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr
430 435 440

TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC
Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala
445 450 455

FIG. 6E



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

29/46

TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA 1504
Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu
460 465 470

AGC CCT CTG ATC CGT CTG CCC ATA GAA CCT GTC TTT GTG GGC ACC 1552
Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Val Phe Val Gly Thr
475 480 485 490

CTC GCT TTC ACA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA 1600
Leu Ala Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala
495 500 505

TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT 1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe
510 515 520

GAC CAT GCA GTG GAT TCT GAC TGAGCCTCA AAGCAGCTCC TGGAGTCAA 1699
Asp His Ala Val Asp Ser Asp
525

TGGCTGCTTA GAGTCAGCCT GGGTGGCACC AGGCCATGCA GGTGAAGTGG CTGCCCTCAG 1759

FIG. 6F

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JAN 16 2004
6625

Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

30/46

GAAATACAAC TAACTAAAAT CAAACACACTA GGTCAACGTGC CTCTCAAATA CTGATTCTG 1819
CCACAGCACC TCTTGAGGCA TCCCCTGGCT ATTCTGTGCA TATTGTTCTT CAGAGACCTC 1879
ACTACCCACA TGCTTGATCTA TTGGGGAAACA GAGAAGAGAC AGGCCACTAA GGTCAAGGCTC 1939
TTTATTTAA GTTCCCCAGA GGAAAGAGTAA GTTGAGAAGG TATCAGTTA ATGTTGAAGA 1999
ATTGACCTCA GGGCTCAGTT TCCATTCCC TCCCTCAGTA TTCTTCCTGG CAAGATAACCC 2059
ATTAAGCAT TCGCCAATCA GAATCTCATT TTATAGTTT TCCCATTGGT CTTTAACCAA 2119
GACTTTCTTG TAGCAATCTC GTAAGCAGTG AACCCCCCTCA GATCAGTAGA ATATAGTATC 2179
TGGGGAGAA GACTTACTTC CTTCAAGGGCA GCAGGCCACAG CCAGGCTCT GTCAACAGG 2239
TAGATCCGA AGCACAGAGA CATAAAAAG GTCTCCCAGA AAACTATAGA CCATTCTCCA 2299
AGTGGAAATTTC CCACCTAGGG CTCTGGTCAC TAGATTGCAA CCTGTGTGTT TGTCATCATC 2359
CTCATCTCAC CATGTATTG CTATGCCCTC CCATAAAAC ACATTGATCC CTAGCAAGAT 2419

FIG. 6G



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCELIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

31/46

TATTGCATTC CAGATTAC TGCTTTGCT AGGCTTTGC TTGCAAAGG GCTGACTTTC 2479

CATTGTTATC ATGGGTATA TATTTTGTC ACCATTCCCA CAAGTAACT TGATGTTGTC 2539

ATAGAACGAA CATCCTACTC TATGATTAC TAACCAATTAA CTTTCCCAGA TCATAGACCT 2599

CTCTGCATAG TAGTCATAGG TCTTGACTTT GGGGAAAGAA AAGGAAGCTG CAGGAATATT 2659

TATCTCCAAA GTCGAATGAG AAAGGAACCTCC AGCAAAATCCA ATGGCTACAA ACTAAAAATC 2719

AGCATTATT CATATTGCTG TTTCTTAGCT GAATATGGAA TAAAGAACTA TTATTATT 2779

TtGAAAAAA AAAAAGAA 2797

FIG. 6H



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

32/46

GGCGGCCGT TTTCCCTGTT CCTGGTCAAC AAAGAAATGT GGAGTGTCTT GGCTGAATCC 60

TCATACAGAC AAGATCATTA TGGTGCTGTT AGGTAGGACT TGTATCCAGA TGTAAGGGTG 120

AAAAGTGT ATAATAAAGG AACCAAGGAG AAAATTGAGA AGGAAAGAAA AAATTGGCCTC 180

TGCAGGGTGT CGAGCAGGAT TGCTTCTGCA ACAAAAGCCT CCACCCAGCC ACATCTTGGG 240

AAAAGA ATG GCC ACT TCT TGG GGC ACA GTC TTT TTC ATG CTG GTG GTA 288
Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val
1 5 10

TCC TGT GTT TGC AGC GCT GTC TCC CAC AGG AAC CAG CAG ACT TGG TTT 336
Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe
15 20 25 30 35

GAG GGT ATC TTC CTG TCT TCC ATG TGC CCC ATC AAT GTC AGC GCC AGC 384
Glu Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser
35 40 45

ACC TTG TAT GGA ATT ATG TTT GAT GCA GGG AGC ACT GGA ACT CGA ATT 432
Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile
50 55 60

FIG. 7A



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEAR ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

33/46

CAT	GTT	TAC	ACC	TTT	GTC	CAG	AAA	ATG	CCA	GGA	CAG	CTT	CCA	ATT	CTA	480	
His	Val	Tyr	Thr	Phe	Val	Gln	Lys	Met	Pro	Gly	Gln	Leu	Pro	Ile	Leu		
65								70				75					
GAA	GGG	GAA	GTT	TTT	GAT	TCT	GTC	AAG	CCA	GGA	CTT	TCT	GCT	TTT	GTA	528	
Glu	Gly	Glu	Val	Phe	Asp	Ser	Val	Lys	Pro	Gly	Leu	Ser	Ala	Phe	Val		
80								85				90					
GAT	CAA	CCT	AAG	CAG	GGT	GCT	GAG	ACC	GTT	CAA	GGG	CTC	TC	TTA	GAG	GTG	576
Asp	Gln	Pro	Lys	Gln	Gly	Ala	Glu	Thr	Val	Gln	Gly	Leu	Leu	Glu	Val		
95								100				105				110	
GCC	AAA	GAC	TCA	ATC	CCC	CGA	AGT	CAC	TGG	AAA	AAG	ACC	CCA	GTG	GTC	624	
Ala	Lys	Asp	Ser	Ile	Pro	Arg	Ser	His	Trp	Lys	Lys	Thr	Pro	Val	Val		
								115				120				125	
CTA	AAG	GCA	ACA	GCA	GGA	CTA	CGC	TTA	CTG	CCA	GAA	CAC	AAA	GCC	AAG	672	
Ile	Lys	Ala	Thr	Ala	Gly	Leu	Arg	Leu	Leu	Pro	Glu	His	Lys	Ala	Lys		
								130				135				140	
GCT	CTG	CTC	TTT	GAG	GTA	AAG	GAG	ATC	TTC	AGG	AAG	TCA	CCT	TTC	CTG	720	
Ala	Leu	Leu	Phe	Glu	Val	Lys	Glu	Ile	Phe	Arg	Lys	Ser	Pro	Phe	Leu		
								145				150				155	

FIG. 7B



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEAR ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

34/46

GTA	CCA	AAG	GGC	AGT	GTT	AGC	ATC	ATG	GAT	GGA	TCC	GAC	GAA	GGC	ATA	768
Val	Pro	Lys	Gly	Ser	Val	Ser	Ile	Met	Asp	Gly	Ser	Asp	Glu	Gly	Ile	160
																165
																170
TTA	GCT	TGG	GTT	ACT	GTG	AAT	TTT	CTG	ACA	GGT	CAG	CTG	CAT	GGC	CAC	816
Leu	Ala	Trp	Val	Thr	Val	Asn	Phe	Leu	Thr	Gly	Gln	Leu	His	Gly	His	175
																180
																185
AGA	CAG	GAG	ACT	GTG	GGG	ACC	TTG	GAC	CTA	GGG	GGA	GCC	TCC	ACC	CAA	864
Arg	Gln	Glu	Thr	Val	Gly	Thr	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	190
																195
																200
ATC	ACG	TTC	CTG	CCC	CAG	TTT	GAG	AAA	ACT	CTG	GAA	CAA	ACT	CCT	AGG	912
Ile	Thr	Phe	Leu	Pro	Gln	Phe	Glu	Lys	Thr	Leu	Glu	Gln	Thr	Pro	Arg	210
																215
GGC	TAC	CTC	ACT	TCC	TTC	GAG	ATG	TTT	AAC	AGC	ACT	TAT	AAG	CTC	TAT	960
Gly	Tyr	Leu	Thr	Ser	Phe	Glu	Met	Phe	Asn	Ser	Thr	Tyr	Lys	Leu	Tyr	220
																225
ACA	CAT	AGT	TAC	TTG	GGA	TTT	GGA	TTG	AAA	GCT	GCA	AGA	CTA	GCA	ACC	1008
Thr	His	Ser	Tyr	Leu	Gly	Phe	Gly	Leu	Lys	Ala	Ala	Arg	Leu	Ala	Thr	230
																240
																245
																250

FIG. 7C



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEAR ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

35/46

CTG	GGA	GCC	CTG	GAG	ACA	GAA	GGG	ACT	GAT	GGG	CAC	ACT	TTC	CGG	AGT	1056
Leu	Gly	Ala	Leu	Glu	Thr	Glu	Gly	Thr	Asp	Gly	His	Thr	Phe	Arg	Ser	
255			260							265						270
GCC	TGT	TTA	CCG	AGA	TGG	TTG	GAA	GCA	GAG	TGG	ATC	TTT	GGG	GGT	GTG	1104
Ala	Cys	Leu	Pro	Arg	Trp	Leu	Glu	Ala	Glu	Trp	Ile	Phe	Gly	Gly	Val	
										280						285
AAA	TAC	CAG	TAT	GGT	GGC	AAC	CAA	GAA	GGG	GAG	GTG	GGC	TTT	GAG	CCC	1152
Lys	Tyr	Gln	Tyr	Gly	Gly	Asn	Gln	Glu	Gly	Glu	Val	Gly	Phe	Glu	Pro	
										295						300
TGC	TAT	GCC	GAA	GTG	CTG	AGG	GTG	GTA	CGA	GGA	AAA	CTT	CAC	CAG	CCA	1200
Cys	Tyr	Ala	Glu	Val	Leu	Arg	Val	Arg	Gly	Lys	Leu	His	Gln	Pro		
										310						315
GAG	GAG	GTC	CAG	AGA	GGT	TCC	TTC	TAT	GCT	TCT	TAC	TAT	TAT	GAC	1248	
Glu	Glu	Val	Gln	Arg	Gly	Ser	Phe	Tyr	Ala	Phe	Ser	Tyr	Tyr	Tyr	Asp	
										325						330
CGA	GCT	GTT	GAC	ACA	GAC	ATG	ATT	GAT	TAT	GAA	AAG	GGG	GGT	ATT	TTA	1296
Arg	Ala	Val	Asp	Thr	Asp	Met	Ile	Asp	Tyr	Glu	Lys	Gly	Gly	Ile	Leu	
										340						350

FIG. 7D



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

36/46

AAA	GTT	GAA	GAT	TTT	GAA	AGA	AAA	GCC	AGG	GAA	GTG	TGT	GAT	AAC	TTG	1344
Lys	Val	Glu	Asp	Phe	Glu	Arg	Lys	Ala	Arg	Glu	Val	Cys	Asp	Asn	Leu	365
GAA	AAC	TTC	ACC	TCA	GGC	AGT	CCT	TTC	CTG	TGC	ATG	GAT	CTC	AGC	TAC	1392
Glu	Asn	Phe	Thr	Ser	Gly	Ser	Pro	Phe	Leu	Cys	Met	Asp	Leu	Ser	Tyr	370
ATC	ACA	GCC	CTG	TTA	AAG	GAT	GGC	TTT	GGC	TTT	GCA	GAC	AGC	ACA	GTC	1440
Ile	Thr	Ala	Leu	Leu	Lys	Asp	Gly	Phe	Gly	Phe	Ala	Asp	Ser	Thr	Val	385
TTA	CAG	CTC	ACA	AAG	AAA	GTG	AAC	AAC	ATA	GAG	ACG	GGC	TGG	GCC	TTG	1488
Leu	Gln	Leu	Thr	Lys	Lys	Val	Asn	Asn	Ile	Glu	Thr	Gly	Trp	Ala	Leu	400
GGG	GCC	ACC	TTT	CAC	CTG	TTG	CAG	TCT	CTG	GGC	ATC	TCC	CAT		1530	
Gly	Ala	Thr	Phe	His	Leu	Leu	Gln	Ser	Leu	Gly	Ile	Ser	His		425	
TGAGGCCACG TACTTCCCTTG GAGACCTGCA TTTGCCAACA CCTTTTAAG GGGAGGAGAG 1590																

FIG. 7E



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

37/46

AGCACTTAGT TTCTGAACTA GTCTGGGACA TCCTGGACTT GAGCCTAGAG ATTAGGTTT 1650
ATTAAATTT ACACATCTAA TGTGAAC TGCTAACCA CTCAAAGAGTA CACAGCTGGC 1710
ACCAGAGCAT CACAGAGGC CCTGTGAGCC AAAAAGTATA GTTTTGGAAC TTAACCTTGG 1770
AGTGAGGCC CAGGGACAGG TCCCCTGGAAA CCAAAGAAAA ATCGCATTTC ACCCCTTTGA 1830
GTGCCTCAT TCCACTGAATA TTTAAATTTC CCTCTTAAT GGTAAACTGA CTTATTGCAA 1890
TCCCAAGACC CATCAAATATC AGTATTTTT TCCTCCCTAT ACAGTGCCT GCCTACCCCTT 1950
ATCTGCACCC ACCTCCCCCTG AAAAGAGAG AAAAAGAAAA AAAAAGAAA AAAAAGAAA 1998

FIG. 7F



**Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS**

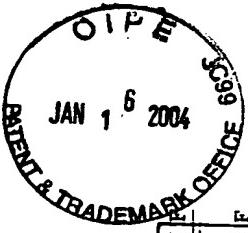
Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

38/46

		ACR
CD39L2	61	K W H R A T A T Q A F F S S I T R A A P P G A R W G Q Q A H - S P L G T A A D G H E V F Y G I M F D A G S T G T R V H V F Q
CD39L4	7	T V F F M L V V S C V C S A V S H R N Q Q T W F E G I F L S S M C P I N V S A S T L Y G I M F D A G S T G T R I H V Y T
CD39L1	1	- - - M A G K V R S L L P P L L A A A G G L L L C V P T R D V R E P P A L K Y G I V L D A G S S H T S M F I Y K
CD39L3	16	K A L Y R T P T I I A L V V L L V S I V V L V S I T V I Q I H K Q E V L - P P G L K Y G I V L D A G S S R T T V Y V Y Q
CD39	7	S N V K T F C S K N I L A I I G F S S I I A V I A L L A V G L T O N K A L P E N V K Y G I V L D A G S S H T S L Y I Y K

FIG. 8A



**Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS**

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

39/46

ACR II

CD39L2	178.	V L K A T A G L R L L - - - P G E K A Q K L L Q K V K E V F K A S P F L V G D D C V S I M N G T D E G V S A W I T I N
CD39L4	126	V L K A T A G L R L L - - - P E H K A K A L L F E V K E I F R K S P F L V P K G S V S I M D G S D E G I L A W V T V N F
CD39L1	118	Y L G A T A G M R L L N L T N P E A S T S V I M A V T H T L T Q Y P F - - D F R G A R I L S Q G Q E G V F G W V T A N Y
CD39L3	135	H L G A T A G M R L L R L Q N E T A A N E V V L E S I Q S Y F K S Q P F - - D F R G A Q L I S Q G Q E E G V Y G W I T A N Y
CD39	127	Y L G A T A G M R L L R M E S E E L L A D R V I L D V V E R S L N Y P F - - D F Q G A R I I T G Q E E G A Y G W I T I N Y

		ACRIV
CD39L2	235	<u>L T G S L</u> - - - - - <u>K T P G G S S V G M</u> <u>D L G G G S T Q I A F L P R V E G T L Q A S P P G Y L T A L R M</u>
CD39L4	183	<u>L T G Q L</u> - - - - - <u>H G H R Q E T V G T L D L G G A S T Q I T F L P Q F E K T L E Q T P R G Y L T S F E M</u>
CD39L1	176	<u>L L E N F I K Y G W G R W F</u> - - <u>R P R - K G T L G A M D L G G A S T Q I T F E T T S P A E D R A S E</u> - - <u>V - Q L H L</u>
CD39L3	193	<u>L M G N F L E K N L W H M W V</u> - - <u>H P H G V E T T G A L D L G G A S T Q I S F V A G E K M D L N T S D</u> - - <u>I M Q V S L</u>
CD39	185	<u>L L G K F S Q K T R W F S S I V P Y E T T N N Q E T F G A L D L G G A S T Q V T F V P Q N Q T I E S P D N</u> - - <u>A L Q F R L</u>

CD39L2	283	<u>F N R T Y K L Y S Y S Y L G L M S A R L A I L G G V E Q P A K D G K E L V S P C L S P S F K G E W E H A E V T Y R</u>
CD39L4	231	<u>F N S T Y K L Y T H S Y S Y L G F G L K A A R L A T L G A L E T E - G T D G H T F R S A C L P R W L E A E W I F G G V K Y Q</u>
CD39L1	229	<u>Y G Q H Y R V Y T H S F L C Y G R D Q V L Q R L L - A S A L Q - - - T H G F H P C W P R G F S T Q V L L G D V Y Q S</u>
CD39L3	248	<u>Y G Y V Y T L Y T H S F Q C Y G R N E A E K K F L - A M L L Q N S P T K N H L T N P C Y P R D Y S I S F T M G H V F D S</u>
CD39	242	<u>Y G K D Y N V Y T H S F L C Y G K D Q A L W Q K L - A K D I Q V A S N E I - L R D P C F H P G Y K K V V N V S D L Y K T</u>

FIG. 8B

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JAN 1 2004
MATERIALS & TRADEMARK OFFICE 6605

Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

40/46

CD39L2	343	V S G Q K A A A S L H E L C A A R V S E V L Q N R V H R T E E V K H V D F Y A F S Y Y Y D L A A G V G L I D A E K G G S
CD39L4	290	Y G G N Q E G E V G F E P C Y A E V L R V V R G K L H Q P E E V Q R G S F Y A F S Y Y Y D R A V D T D M I D Y E K G G I
CD39L1	283	P C T M A Q R P Q N F N S S A R V S L S G S S D P H L C R D L V S G L F S F S S C - P F S R C S F N G V F Q O P P V A G N
CD39L3	307	L C T V D Q R P E S Y N P N D V I T F E G T G D P S L C K E K V A S I F D F K A C H D Q E T C S F D G V Y Q P K I K G P
CD39	300	P C T - - K R F E M T L P F Q Q F E I Q G I G N Y Q Q C H Q S I L E F N T S Y C - P Y S Q C A F N G I F L P P L Q G D
CD39L2	403	L V V G D F P E I A A K Y V C R T L E T Q P Q S S P F S C M D L T Y V S L L L Q E - F G F P R S K V L K L T R K I D N V E
CD39L4	350	L K V E D F E R K A R E V C D N L E N F T S G S P F L C M D L S Y I T A L L K D G F G F A D S T V L Q L T K K V N N I E
CD39L1	342	F V - - - - A F S A F F Y T V D F L R T S M G L P V A T L Q Q L E A A A V N V C N Q T W A Q - - - - -
CD39L3	367	F V - - - - A F A G G F Y Y T A S A L N L S G S F - - S L D T F N S S T W N F C S Q N W S Q L P L L P K F D E V Y
CD39	357	F G - - - - A F S A F Y F V M K F L N L T S - - E K V S Q E K V T E M M K K F C A Q P W E E I K T S Y A G V K E Y
CD39L2	462	T S W A L G A I F H Y I D S L N R Q K S P A S *
CD39L4	410	T G W A L G A T F H L L Q S L G I S H
CD39L1	384	- - - - - Q L L S R G Y G F D E R A F G G V I F Q K K A A D T A V G W A L G Y M L N L T N L I P A D P P G
CD39L3	418	A R S Y C F S A N Y I Y H L F V N G Y K F T E E T W P Q I H F E K E V G N S S I A W S L G Y M L S L T N Q I P A E S P L
CD39	409	L S E Y C F S G T Y I L S L L Q G Y H F T A D S W E H I H F I G K I Q S D A G W T L G Y M L N L T N M I P A E Q P -

FIG. 8C



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEAR ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

41/46

CD39L2	485	
CD39L4	429	
CD39L1	432	<u>L R K G T D F S S W V V L L L F A S A L L A A L V L L R Q V H S A K L P S T I *</u>
CD39L3	478	<u>I R L P I E P P V F V G T L A F F T V A A L L C L A F P L A Y L C S A T R R K R H S E H A F D H A V D S D *</u>
CD39	468	<u>L S T P L S H S T Y V F L M V L F S L V L F T V A I G L L I F H K P S Y F W K D M V *</u>

FIG. 8D



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS

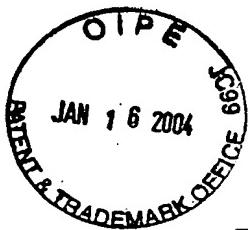
Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

42/46

peaGDP	1	- - - - - M
potapyrase	1	- - - - - M <u>L</u> <u>N</u> <u>Q</u> <u>N</u>
CD39L2	1	M K K G I R Y E T S R K T S Y I F Q Q P Q H G P W Q T R M R K I S N H G S L R V A K V A Y P L G L C V G V F I Y V A Y I
CD39L4	1	- - - - - M A T S W G
dNTPase	1	- - - - - M K Y E Y K L L A T D E K P P R R K S S G S P N A S S G G N R G P S G L
yGDPase	1	- - - - - K T P E
ACRI 		
peaGDP	2	E L L I K L I T F L L F S M P A I T S S Q Y L G N N L - L T S R K I F L K Q E E I S S Y A V V F D A G S T G S R I H V Y
potapyrase	6	S H F I F I I L I A I F L V L P L S L L S K N V N A Q I - P L R R H L L S H E S E - - H Y A V I F D A G S T G S R V H V F
CD39L2	61	K W H R A T A T Q A F F S I T R A A P G A R W G Q Q A - H - S P L G T A A D G H E V F Y G I M F D A G S T G T R V H V F
CD39L4	7	T V F F M L V V S C V C S A V S H R N Q Q T W P E G I - F L S S M C P I N V S A S T L Y G I M F D A G S T G T R V H V Y
dNTPase	37	K I S F L C L I I S V I I L L F V F G F V S E N A S P - Y L A R L A S K F G Y S K V Q Y A A I I D A G S T G S R V L A Y
yGDPase	5	D I S I L P Y N D E P G Y L Q D S K T E Q N Y P E L A D A V K S Q T S Q C S E E H K Y V I M I D A G S T G S R V H V I Y

FIG. 9A



Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEAR ACIDS

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

43/46

ACR II

peaGDP	61	<u>H F N Q N D L L H I G K G V E Y Y N K I T P G L S S Y A N N P E Q A A K S L I P P L E Q A E D V V P D D L Q P P T P V</u>
potapyrase	63	<u>R F D E K L G L L P I G N N I E Y F M A T E P G L S S Y A E D P K A A A N S L E P L L D G A E G V V P Q E L Q S E T P L</u>
CD39L2	119	<u>Q F T - R P P R E T P T L T H E T F K A V K P G L S A Y A D D V E K S A Q Q G I R E L L D V A K Q D I P F D F W K A T P L</u>
CD39L4	66	<u>T F V Q K M P G Q L P I L E G E V F D S V K P G L S A F V D Q P K Q G A E T V Q G L L E V A K D S I P R S H W K K T P V</u>
dNTPase	96	<u>K F N R S F I D N K L V L Y E E L F K E R K P G L S S F A D N P A E G A H S I K L L I D E A R A F I P K E H W S S T P L</u>
yGDPase	65	<u>K F D - - V C T S P P T L L D E K F D M L E P G L S S F D T D S V G A A N S L D P L L K V A M N Y V P I K A R S C T P V</u>

ACR III

peaGDP	121	<u>R L G A T A G L R L L N G D A S E K I L Q S V R D M L S S N R S T F - N V Q P D A V S I I D G T Q E G S Y L W V T V N Y A</u>
potapyrase	123	<u>E L G A T A G L R M L K G D A A E K I L Q A V R N L V K N Q S T F - H S K D Q W V T I L D G T Q E G S Y M W A A I N Y L</u>
CD39L2	178	<u>V L K A T A G L R L L P G E K A Q K L L Q K V K E V F K - A S P F - L V G D D C V S I M N G T D E G V S A W I T I N F L</u>
CD39L4	126	<u>V L K A T A G L R L L P E H K A K A L L F E V K E I F R - K S P F - L V P K G S V S I M D G S D E G I L A W V T V N F L</u>
dNTPase	156	<u>V L K A T A G L R L L P A S K A E N I L N A V R D L F A - K S E F - S V D M D A V E I M D G T D E G I F S W F T V N F L</u>
yGDPase	123	<u>A V K A T A G L R L L G D A K S S K I L L S A V R D H L E K D Y P F P V V E G D G V S I M G G D E E G V F A W I T T N Y L</u>

FIG. 9B



**Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS**

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

44/46

ACR IV

PeaGDP	180	<u>LGNLGGK</u> <u>KYT</u> <u>K</u> - - <u>TVGVID</u> <u>LGGSVQ</u> <u>MAYAVSK</u> <u>KTAKNAPKVADGDPPYIKKVVVLKGIPYD</u>
Potapyrase	182	<u>LGNLGGKD</u> <u>YKS</u> <u>=</u> - <u>TATIDLGGSVQ</u> <u>MAYAISNEQFAKAPQNEDG</u> <u>=EPYVQQKHLMSSKDYN</u>
CD39L2	236	<u>TGSLKTPGGS</u> <u>=</u> - <u>SVGMLDLGGSTQIAFLPRVEG</u> <u>=- - - TLQASPPPGYLTALRMFNRTRYK</u>
CD39L4	184	<u>TGQLHGHROE</u> <u>=</u> - <u>TVGTLDLGGASTQITFLPQEKF</u> <u>=- - - TLEQTPRGYLTSFEMFNSTYK</u>
dNTPase	214	<u>LGRLSKTNQA</u> <u>=</u> - <u>AA-</u> - <u>LDLGGSSTQVTFSPTD</u> <u>PD</u> <u>=- - - QVPVYDK</u> <u>- YMHEVVTSSKKIN</u>
YGDase	183	<u>LGNIGANGPKLPTAAVFD</u> <u>LGGSSTQIVFEPTEFPINEKMV</u> <u>=- - - DGEEHKFDLKFGDENY</u>

FIG. 9C



**Title: METHODS AND COMPOSITIONS RELATING TO
CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS**

Applicants: Brian Paul Chadwick et al.

Docket No.: 28110/36120A

45/46

PeaGDP	276	TYS GEE <u>E</u> KATA T <u>S</u> G - ANF N <u>KCNTIRKALKLNYPCPYQONCTFGGIWNGG - - <u>G</u>GNGQKN</u>
potapyrase	277	SYGGV D <u>V</u> KVKAPKKG - SSWKR C RRLTRHALKINA <u>K</u> CNIEECTFNGVWNGG - - <u>G</u> G D G Q K N
CD39L2	335	EHAEV T <u>V<u>T</u>YRVSGQKAASLHE<u>L</u>CAAR - - VSEV<u>E</u> - - - LQNRV - - - HRT - - EEVKHVD</u>
CD39L4	282	I F <u>G</u> G V K <u>V</u> KYQYGGNQE G E V GF E P C Y A E - - VL R V - - - VRGKL - - - HQP - - EEV Q RGS
dNTPase	308	T Y <u>G</u> N V Q YKVSGKENG K <u>S</u> SAE Q OPIVDFFD A CLEL - - - VKS K V M PL V KPKP - - FTLKQ H A
Y GDPase	298	LESKE T <u>T<u>I</u>DFIGPDEPSGAQCRPLTDEILNKDAQCQSPPCSFNGVHQPSLUVRTFKESND</u>
PeaGDP	332	LF A <u>S<u>S</u>FFFYLPEDTGMVDASTPNFILRPVDIETTAKEACALNFEDAKSTYPFLDKKKNVAS</u>
potapyrase	333	I H <u>A<u>S<u>S</u>FFFYDIGAQVGIVDTKFPSALAKPIQYLNAAKVACQTNVADIKSIFPKTQDRNI - P</u></u>
CD39L2	379	FYAFSYYD L AAGVGLIDAE - KGG S LV V GDFEIAAKYVCRT - - - - - LETQPPQSSSP
CD39L4	326	FYAFSYYDRAVDTDMIDYE - KG G GILKVED F ERKAREVCDN - - - - - LENFTSGSP
dNTPase	360	YAAF S YYFERAIESGLV D PL - AGGETTVEAYRKKAQEI CAI - - - - - P N DE - - QP
Y GDPase	358	IYIF S YYFYDRT R PLGMPLSFTLNELNDLARI V KGEET W NSEVF S GIAGS L - - - - - DELESDS

FIG. 9D



Title: METHODS AND COMPOSITIONS RELATING TO
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Docket No.: 28110/36120A

46/46

peaGDP	392	<u>Y V C M D L I Y Q Y V L L V D G F G L D P L Q K I T S G K E I E Y Q D A I V E A A W P L G N A V E A I S A L P K F E R L</u>
potapyrase	392	<u>Y L C M D L I Y E Y T L L V D G F G L N P H K E I T V I H D V Q Y K N Y L V G A A W P L G C A I D L V S S T T N K I R V</u>
CD39L2	428	<u>F S C M D L T Y V S L L Q E - F G F P R S K V L K L T R K I D N - - - V E T S W A L G A I F H Y I D S L N R Q K S P</u>
CD39L4	375	<u>F L C M D L S Y I T A L L K D G F G F A D S T V L Q L T K K V N N - - - I E T G W A L G A T F H L L Q S L G I S H</u>
dNTPase	406	<u>F M C F D L T F I S T L L R E G F G L N D G K K I K L Y K K I D G - - - H E I S W A L G C A Y N V L T S D E K F S N S</u>
yGDPase	415	<u>H F C L D L S F Q V S L L H T G Y D I P L Q R E L R T G K K I A N K - - - E I G W C L G A S S L P L L K A D N W K C K I</u>

peaGDP	452	M Y F V
potapyrase	452	<u>A S S *</u>
CD39L2	483	<u>A S *</u>
CD39L4	429	
dNTPase	462	
yGDPase	471	<u>Q S A</u>

FIG. 9E